

Amendments to the Specification:

Amendments to the specification are shown below.

****Please note that because there was underlining in the original text, additions are noted herein by Double Underlining.****

· On pages 8 to 9, replace the paragraph beginning at page 8, line 20 and ending at page 9, line 3 with the following replacement paragraph:

--Figure 1 shows an overview of the secondary and tertiary structure of the GTPase activating region RNA from *Thermotoga maritima*: a) RNA secondary structure derived from the crystal structure (RNA sequence is SEQ ID NO: 5). Lines indicate long-range base triples and the long-range 1088-1060 base pair; b) ribbon-and-stick schematic of the RNA tertiary structure (For clarity, protein L11 has been omitted from view); c) same as (b), but the view is down the major groove of the 1095 stem to emphasize the compactness of the RNA fold. Figures 1b and 1c were made with the program RIBBONS (Carson, 1991).--

· On page 10, replace the paragraph at lines 9-21 with the following replacement paragraph:

--Figure 4 shows the RNA-L11 complex within the GTPase activating region from *Thermotoga maritima*: a) alignment of four widely divergent L11 sequences (“E coli” is Escherichia coli, SEQ ID NO: 1; “T marit” is Thermotoga maritima, SEQ ID NO: 2; “Sulf ac” is Sulfolobus acidocaldarius, SEQ ID NO: 3; and “Sacc cor” is Saccharomyces cerevisiae, SEQ ID NO: 4), together with a schematic of the protein’s secondary structure. The sidechains of residues ~~colored green~~ shown in forward-slanting narrow hatch marks participate in the hydrophobic core in the crystal structure. Residues involved in RNA binding are shown with backward-slanting narrow hatch marks ~~colored blue~~ for side-chain contacts, backward slanting wide hatch marks ~~red~~ for main-chain contacts, or cross-hatched ~~purple~~ if both the side-chain and main-chain interact with RNA. Abbreviations: E. coli, *Escherichia coli* (eubacterium); T. marit, *Thermotoga maritima* (eubacterium); Sulf ac, *Sulfolobus acidocaldarius* (archaea) ; Sacc cer, *Saccharomyces cerevisiae* (eukaryote). The numbering is based on the *Thermotoga maritima* sequence present in the crystal structure. b) stereoview of the complex. The L11 N- and C-terminal domains are labeled. Note that the N-terminal domain straddles the interface of the 1067 and 1095 stem-loops. c) orthogonal stereoview of the complex. This view emphasizes the relatively loose

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association of the L11 N-terminal domain with the RNA. Figures 4b and 4c were made with RIBBONS (Carson, 1991).--